



#4/a

-1-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: CHOU, Tau-San
EISENREICH, Robert
SANFORD, John
BLOWERS, Alan
SMITH, Franzine
VAN ECK, Joyce
- (ii) TITLE OF INVENTION: PRODUCTION OF TRANSGENIC POINSETTIA
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/903,944
 - (B) FILING DATE: 31-JUL-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: GRANADOS, Patricia D.
 - (B) REGISTRATION NUMBER: 33,683
 - (C) REFERENCE/DOCKET NUMBER: 89166/107
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)672-5300
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 - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15

Val Gly Glu Ile Met Asn Ser
20

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Met Ala Ser Lys Ala Gly Ala Ile Ala Gly Lys Ile Ala Lys Val
 1 5 10 15

Ala Leu Lys Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala Phe
 1 5 10 15

Val Lys Ile Leu Asn Ser
 20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys Ile
 1 5 10 15

Ala Gly Lys Ile Ala
 20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Lys Leu
1 5 10 15
Ala Arg Lys Ile Ala Arg Leu Gly Val Ala Phe
20 25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..72

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GGC ATC GGA AAG TTC CTT CAC AGT GCA AAG AAG TTC GGA AAG GCC 48
Met Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala
1 5 10 15
TTC GTG GGT GAG ATC ATG AAC AGT TAA 75
Phe Val Gly Glu Ile Met Asn Ser
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala
1 5 10 15
Phe Val Gly Glu Ile Met Asn Ser
20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..69

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GGA ATC GGC AAG TTC CTC AAG AGC GCA AAG AAG TTT GGC AAG GCC	48
Met Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala	
1 5 10 15	
TTC GTG AAG ATC CTG AAC TCC TAA	72
Phe Val Lys Ile Leu Asn Ser	
20	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala	
1 5 10 15	
Phe Val Lys Ile Leu Asn Ser	
20	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..66

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AAG ATC GCC GGA AAG ATA GCA AAG ATT GCG GGG AAA ATC GCG AAG	48
Met Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys	
1 5 10 15	
ATC GCT GGC AAA ATC GCG TAA	69
Ile Ala Gly Lys Ile Ala	
20	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys
 1 5 10 15
 Ile Ala Gly Lys Ile Ala
 20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..81

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AAG AGG AAG CGT GCA GTT AAG AGG GTG GGA CGT CGA TTG AAG CTT 48
 Met Lys Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Leu
 1 5 10 15
 GCA AGA AAG ATC GCA AGG CTC GGT GTG GCT TTC TAA 84
 Ala Arg Lys Ile Ala Arg Leu Gly Val Ala Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Leu
 1 5 10 15
 Ala Arg Lys Ile Ala Arg Leu Gly Val Ala Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..117

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG	CTT	CTC	GCT	ATT	GCC	TTC	TTG	GCA	TCA	GTT	TGC	GTG	TCT	TCC	ATG	48
Met	Leu	Leu	Ala	Ile	Ala	Phe	Leu	Ala	Ser	Val	Cys	Val	Ser	Ser	Met	
1				5				10						15		
GGC	ATC	GGA	AAG	TTC	CTT	CAC	AGT	GCA	AAG	AAG	TTC	GGA	AAG	GCC	TTC	96
Gly	Ile	Gly	Lys	Phe	Leu	His	Ser	Ala	Lys	Lys	Phe	Gly	Lys	Ala	Phe	
			20					25					30			
GTG	GGT	GAG	ATC	ATG	AAC	AGT	TAA									120
Val	Gly	Glu	Ile	Met	Asn	Ser										
			35													

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Leu	Leu	Ala	Ile	Ala	Phe	Leu	Ala	Ser	Val	Cys	Val	Ser	Ser	Met
1				5				10						15	
Gly	Ile	Gly	Lys	Phe	Leu	His	Ser	Ala	Lys	Lys	Phe	Gly	Lys	Ala	Phe
			20					25					30		
Val	Gly	Glu	Ile	Met	Asn	Ser									
			35												

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..108

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG	CTT	CTC	GCT	ATT	GCC	TTC	TTG	GCA	TCA	GTT	TGC	GTG	TCT	TCC	GGA	48
Met	Leu	Leu	Ala	Ile	Ala	Phe	Leu	Ala	Ser	Val	Cys	Val	Ser	Ser	Gly	
1				5				10					15			
ATG	GCC	TCT	AAG	GCA	GGT	GCT	ATC	GCC	GGC	AAA	ATC	GCG	AAG	GTG	GCA	96
Met	Ala	Ser	Lys	Ala	Gly	Ala	Ile	Ala	Gly	Lys	Ile	Ala	Lys	Val	Ala	
			20				25					30				
TTG	AAG	GCC	CTT	TAA												111
Leu	Lys	Ala	Leu													
			35													

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Leu	Leu	Ala	Ile	Ala	Phe	Leu	Ala	Ser	Val	Cys	Val	Ser	Ser	Gly
1				5				10					15		
Met	Ala	Ser	Lys	Ala	Gly	Ala	Ile	Ala	Gly	Lys	Ile	Ala	Lys	Val	Ala
			20				25					30			
Leu	Lys	Ala	Leu												
			35												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..114

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG	CTT	CTC	GCT	ATT	GCC	TTC	TTG	GCA	TCA	GTT	TGC	GTG	TCT	TCC	ATG	48
Met	Leu	Leu	Ala	Ile	Ala	Phe	Leu	Ala	Ser	Val	Cys	Val	Ser	Ser	Met	
1				5				10					15			

GGA ATC GGC AAG TTC CTC AAG AGC GCA AAG AAG TTT GGC AAG GCC TTC 96
Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala Phe
20 25 30

GTG AAG ATC CTG AAC TCC TAA 117
Val Lys Ile Leu Asn Ser
35

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Met
1 5 10 15
Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala Phe
20 25 30
Val Lys Ile Leu Asn Ser
35

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..108

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG CTT CTC GCT ATT GCC TTC TTG GCA TCA GTT TGC GTG TCT TCC AAG 48
Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Lys
1 5 10 15
ATC GCC GGA AAG ATA GCA AAG ATT GCG GGG AAA ATC GCG AAG ATC GCT 96
Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala
20 25 30
GGC AAA ATC GCG TAA 111
Gly Lys Ile Ala
35

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Lys
 1             5             10             15
Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala
      20             25             30
Gly Lys Ile Ala
      35
```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..126

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
ATG CTT CTC GCT ATT GCC TTC TTG GCA TCA GTT TGC GTG TCT TCC AAG      48
Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Lys
 1             5             10             15
AGG AAG CGT GCA GTT AAG AGG GTG GGA CGT CGA TTG AAG AAG CTT GCA      96
Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Lys Leu Ala
      20             25             30
AGA AAG ATC GCA AGG CTC GGT GTG GCT TTC TAA      129
Arg Lys Ile Ala Arg Leu Gly Val Ala Phe
      35             40
```

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Lys
1 5 10 15
Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Lys Leu Ala
20 25 30
Arg Lys Ile Ala Arg Leu Gly Val Ala Phe
35 40